**PAPER • OPEN ACCESS**

# Stability Analysis Susceptible, Exposed, Infected, Recovered (SEIR) Model for Spread Model for Spread of Dengue Fever in Medan

To cite this article: Syafruddin Side *et al* 2018 *J. Phys.: Conf. Ser.* **954** 012018

View the article online for updates and enhancements.

# Stability Analysis Susceptible, Exposed, Infected, Recovered (SEIR) Model for Spread Model for Spread of Dengue Fever in Medan

**Syafruddin Side[1*], Yulita Molliq Rangkuti[2], Dian Gerhana Pane[2], Marlina Setia Sinaga[2]**

[1]Department of Mathematics, Faculty of Mathematics and Natural Science, Universitas Negeri Makasar, (UNM), Makasar, South Sulawesi, Indonesia
[2]Department of Mathematics, Faculty of Mathematics and Natural Science, Universitas Negari Medan, UNIMED, 20221, Medan, North Sumatera, Indonesia

*syafruddin@unm.ac.id

**Abstract.** Dengue fever is endemic disease which spread through vector, Aedes Aegypty. This disease is found more than 100 countries, such as, United State, Africa as well Asia, especially in country that have tropic climate. Mathematical modeling in this paper, discusses the speed of the spread of dengue fever. The model adopting divided over four classes, such as Susceptible (S), Exposed (E), Infected (I) and Recovered (R). SEIR model further analyzed to detect the re-breeding value based on the number reported case by dengue in Medan city. Analysis of the stability of the system in this study is asymptotically stable indicating a case of endemic and unstable that show cases the endemic cases. Simulation on the mathematical model of SEIR showed that require a very long time to produce infected humans will be free of dengue virus infection. This happens because of dengue virus infection that occurs continuously between human and vector populations.

*Keywords*: SEIR model; Endemic; Runge-Kutta method; Stability; Dengue fever

## 1. Introduction

Dengue Fever Disease (DFD) is not a new disease because it happens almost every year in line with the changing seasons, from rainy season to the dry season. Based on data from the North Sumatra Health Office (DHO Sumatra), cases of DFD in 2013, there are 33 district / cities in North Sumatra Province reached 4,746 people. DFD patients in Medan are 1,270 people. From January to October 2014, the the number of dengue cases as many as 1068 cases and there are nine people died from dengue fever in the city of Medan. Based on the data, from 21 districts there are two districts that have increased the number of DFD patients in 2013 to 2014. In the Medan Helvetia sub-district, there were 101 patients and two of them died in 2013. It increases in January to October 2014, there were 104 patients and one person died. Whereas in sub-district of Medan Sunggal, there were 83 patients with DFD in 2013. Meanwhile, in January to October 2014 increased dengue fever which is reached 103 people. The high cases of dengue fever is important to investigate. Lack of awareness for Clean and Healthy Lifestyle that have not been executed so the vector is found in many areas.

A mathematical model can be applied to determine the amount of the spread of dengue fever in the city of Medan. With the development of science of mathematics, mathematical models helped provide an important role in preventing the spread of dengue fever. Meanwhile, the model is built to

look for the amount of the spread of dengue disease. The mathematical model can also assist in the prediction of epidemic control in the future in order to avoid endemic. After many years, the more complex models have been derived by [1]. In some diseases, have been found for a specified period, part of the class Exposed population is infected with the disease but cannot transmit. For modeling the disease is called SEIR models used [2]. In the model of SEIR, the population is divided into four classes: class vulnerable populations ($S$), in which all individuals are susceptible to the disease; class exposed population ($E$), in which all individuals who are infected but not yet infectious; class population is infected ($I$), where all the people infected by the disease and can transmit; and class populations recovered ($R$), where individual cured [3]. Many of the researchers who discussed the model of SEIR with a variety of problems, some of them are [4] studied the stability of the global era is structured in SEIR Model with infectivity in the latency period. [5] discussed the dynamic behavior of the epidemic SEIR system with nonlinear transmission rate. [6] discussed the global stability of SEIR models with vertical transmission and saturated contact rate [7] also  [8] discussed about SEIR model.

Mathematical model of the spread of dengue fever that is discussed in this paper is a dynamic model with a mathematical model, that are SIR and SEIR. SIR and SEIR model are one of the mathematical model to analyze the spread of one serotype of dengue virus between humans by vector. Then simulation model of the spread of measles to the effect of vaccination using Maple program was applied. The analysis results will be obtained parameters are most influential in the spread of measles is the rate of transmission. Thus the spread of measles epidemic can be controlled by adding a vaccination program [9]. [10,11] make a stability analysis of differential equation model. [12] and [13] conducted research on the SIR model for transmission of dengue in South Sulawesi, Indonesia and Selangor, Malaysia. [14] also conducted research on the model of SEIR for transmission of dengue with simulation. In tropical countries and become the biggest disease epidemic in Southeast Asia. Thus epidemics caused by climate change and the lack of knowledge and awareness of people about dengue so that dengue fever is endemic for a long time. In this paper, SEIR model adopted by [14] and applied for Medan city.

**2. Stabilty Analysis of Model**

*2.1 SEIR Model of Dengue Fever*

The SEIR model of dengue fever adopted by [13]. The model for the human and mosquito populations follows:

$$\frac{dS_h}{dt} = \mu_h N_h - \left(\frac{\beta_h b I_v}{N_h} + p + \mu_h\right)S_h, \tag{1}$$

$$\frac{dE_h}{dt} = \left(\frac{\beta_h b I_h}{N_h} + p\right)S_h - (\mu_h + \varphi_h)E_h, \tag{2}$$

$$\frac{dI_h}{dt} = \varphi_h E_h - (\mu_h + \gamma_h + \alpha_h)I_h, \tag{3}$$

$$\frac{dE_v}{dt} = \frac{\beta_v b I_h}{N_h}S_v - (\mu_v + \delta_v)E_v, \tag{4}$$

$$\frac{dI_v}{dt} = \delta_v E_v - \mu_v I_v. \tag{5}$$

The rate of change in human and vector populations are constant, so that:

$$N_h = S_h + E_h + I_h + R_h,$$

$$N_v = A\mu_v = S_v + E_v + I_v.$$

$$N_v - E_v - I_v = A\mu_v - E_v - I_v.$$

*2.2 Equilibrium Point*

To find the point of equilibrium of the system (1)-(5), we simplify the system by assuming:

$$x = \frac{dS_h}{dt} \quad u = \frac{dE_h}{dt} \quad y = \frac{dI_h}{dt}, \quad w = \frac{dE_v}{dt}$$

$$z = \frac{dI_v}{dt} = \frac{I_v}{A/\mu_v}$$

$$N_v = \frac{A}{\mu_v} = S_v + E_v + I_v, \quad \text{and}$$

$$S_v = N_v - E_v - I_v = \frac{A}{\mu_v} - E_v - I_v.$$

we obtained [13]:

$$\frac{dx}{dt} = \mu_h(1 - x) - (p + \alpha z)x, \tag{6}$$

$$\frac{du}{dt} = (p + \alpha z)x - (\mu_h + \varphi_h)u, \tag{7}$$

$$\frac{dy}{dt} = \varphi_h u - (\mu_h + \gamma_h + \alpha_h)y, \tag{8}$$

$$\frac{dw}{dt} = \gamma_v(1 - z - w)y - (\mu_v + \delta_v)w, \tag{9}$$

$$\frac{dz}{dt} = \delta_v w - \mu_v z. \tag{10}$$

where $\gamma_v = \beta_v b$, and $\alpha = \frac{\beta_v b A}{N_h \mu_v}$. With condition $\frac{dx}{dt} = \frac{du}{dt} = \frac{dy}{dt} = \frac{dw}{dt} = \frac{dz}{dt} = 0$, then the system in Eqs. (6)-(10) is simplified by assumtion $a = \mu_h, b = a + p, c = \alpha, d = p, e = a + \varphi_h, f = \varphi_h, \ g = a + \gamma_h + \alpha_h, h = \gamma_v, j = \delta_v + \mu_v, k = \delta_v$, and $l = \mu_v$.

We have

$$a - (b + cz)x = 0 \tag{11}$$
$$(d + cz)x - eu = 0 \tag{12}$$
$$fu - gy = 0 \tag{13}$$
$$h(1(-z - w)y) - jw = 0 \tag{14}$$
$$kw - lz = 0 \tag{15}$$

Thus the system (11)-(15) gained two points of equilibrium by using MAPLE.

*a. The equilibrium point for free- disease of dengue*

Equilibrium point for free-disease $E_0$ is a condition where there are no cases of dengue disease spread between human and vector populations. Equilibrium point can be written $x_0, u_0, y_0, w_0, z_0$. Thus obtained free-disease equilibrium point $E_0$ is obtained as follows:

$$x_0 = \frac{a}{b - cm(\sqrt{q} + n)} \tag{16}$$

$$u_0 = \frac{gjlm(\sqrt{q} + n)}{-fhm(\sqrt{q} + n)(k + l) - fkl} \tag{17}$$

$$y_0 = \frac{jlm(\sqrt{q} + n)}{-hm(\sqrt{q} + n)(k + l) - kh} \tag{18}$$

$$w_0 \;=\; -\frac{m\left(\sqrt{q}+n\right)}{k} \tag{19}$$

$$z_0 \;=\; m\left(\sqrt{q}+n\right) \tag{20}$$

*b.   The equilibrium point for Endemic*

Equilibrium point for endemic is the case of the spread of dengue disease between human and vector. The next set of endemic equilibrium point, symbolized $E_1 = (x_1, u_1, y_1, w_1, z_1)$, we obtained [14] follows:

$$x_1 \;=\; \frac{a}{b + cm\left(\sqrt{q}-n\right)} \tag{21}$$

$$u_1 \;=\; -\frac{gjlm\left(\sqrt{q}-n\right)}{fhm\left(\sqrt{q}-n\right)(k+l) - fl} \tag{22}$$

$$y_1 \;=\; \frac{jlm\left(\sqrt{q}-n\right)}{hm\left(\sqrt{q}-n\right)(k+l) - kh} \tag{23}$$

$$w_1 \;=\; \frac{m\left(\sqrt{q}-n\right)}{k} \tag{24}$$

$$z_1 \;=\; m\left(\sqrt{q}-n\right) \tag{25}$$

where:

$$m = \frac{1}{2c(jleg + hfka + hfla)},$$

$$n = hfkda + hflda - hfkca + jlegb,$$

$$\begin{aligned}
q = \; & (hfkda)^2 + 2kl(hfda)^2 + 2dc(hfka)^2 + \\
& 2hfkdajlegb + (hflda)^2 + 2ldkc(hfa)^2 + \\
& 2hfdajegbl^2 + (hfkca)^2 - 2hfkcajlegb + \\
& (jlegb)^2 + 4hfkdaljgec.
\end{aligned}$$

*2.3 Eigenvalue for SEIR Model*

Having obtained equilibrium point, will then be analyzed stability equilibrium point. The first step there is linearized system of linear equations that arise in models of dengue epidemic.
The equations used in the linearization process is as follows [15]:

$$f(x,u,y,w,z) \;=\; \frac{dx}{dt} \;=\; a - (b + cz)x, \tag{26}$$

$$g(x,u,y,w,z) \;=\; \frac{du}{dt} \;=\; (d + cz)x - eu, \tag{27}$$

$$h(x,u,y,w,z) \;=\; \frac{dy}{dt} \;=\; fu - gy, \tag{28}$$

$$i(x,u,y,w,z) \;=\; \frac{dw}{dt} \;=\; h(1 - z - w)y - jw, \tag{29}$$

$$j(x,u,y,w,z) \;=\; \frac{dz}{dt} \;=\; kw - lz. \tag{30}$$

Linearization that has been done is the Jacobian matrix J.
Jacobian matrix of the system (24)-(29) is:

$$J = \begin{bmatrix} -b-cz & 0 & 0 & 0 & -xc \\ d+cz & -e & 0 & 0 & cx \\ 0 & f & -g & 0 & 0 \\ 0 & 0 & h(1-z-w) & -hy-j & -hy \\ 0 & 0 & 0 & k & -l \end{bmatrix}$$

Eigenvalues obtained if and only if $|J - \lambda I| = 0$. With $J$ is the Jacobian matrix that linearized for endemic equilibrium point, $\lambda$ is eigenvalues and $I$ is the identity matrix. Then the eigenvalues for endemic equilibrium point as follows [13]:

With:

$k_1 = = C_1 C_2 C_3 (C_4 C_5 - C_6),$

$k_2 = = -(C_1 C_2 C_3 (C_4 + C_5) + (C_1 C_2 + C_1 C_3 + C_2 C_3)(C_4 C_5 - C_6)),$

$k_3 = = C_1 C_2 C_3 + (C_4 + C_5)(C_1 C_2 + C_1 C_3 + C_2 C_3) + (C_1 + C_2 + C_3)(C_4 C_5 - C_6),$

$k_4 = = -(C_1 C_2 + C_1 C_3 + C_2 C_3) + (C_1 + C_2 + C_3)(C_4 + C_5)(C_4 C_5 - C_6),$

$k_5 = = C_1 + C_2 + C_3 + C_4 + C_5.$ and

$C_1 = = -b - bc\sqrt{q} + bn,$

$C_2 = = -e, \; C_3 = -g$

$C_4 = = \dfrac{hljm\,(\sqrt{q}-n)}{-kh+hm(\sqrt{q}-n)+(k+l)}, \; C_5 = -l$

$C_6 = = \dfrac{hljmk\,(\sqrt{q}-n)}{-kh+hm(\sqrt{q}-n)+(k+l)}.$

The stiffness matrix of composite sandwich plate is formed by combining the stiffness matrix of the top face sheet with the upper half of honeycomb core and the bottom face sheet with the lower half of honeycomb core.

We obtained Jacobian matrix follow:

$$\begin{pmatrix} -(b+cm(\sqrt{q}-n))-\lambda & 0 & 0 & 0 & -\dfrac{ca}{cm(\sqrt{q}-n)+b} \\ cm(\sqrt{q}-n)+d & -e-\lambda & 0 & 0 & \dfrac{ca}{cm(\sqrt{q}-n)+b} \\ 0 & f & -g-\lambda & 0 & 0 \\ 0 & 0 & h\left(1-m(\sqrt{q}-n)-\dfrac{m(\sqrt{q}-n)}{k}\right) & \dfrac{hlm(\sqrt{q}-n)}{hm(\sqrt{q}-n)(k+l)-kh}-j-\lambda & \dfrac{hlm(\sqrt{q}-n)}{hm(\sqrt{q}-n)(k+l)-kh} \\ 0 & 0 & 0 & k & -l-\lambda \end{pmatrix}$$

$$(-b-bc\sqrt{q}+bn-\lambda)(-e-\lambda)\left[\left(\dfrac{hljm(\sqrt{q}-n)}{-kh+hm(\sqrt{q}-n)(k+l)}-j-\lambda\right)(-l-\lambda)-\left(\dfrac{hljmk(\sqrt{q}-n)}{-kh+hm(\sqrt{q}-n)(k+l)}\right)\right]=0.$$

So that is the characteristic equation can be simplified:

$$k_1 + k_2\lambda + k_3\lambda^2 + k_4\lambda^3 + k_5\lambda^4 - \lambda^5 = 0.$$

The conclusion of the eigenvalues is,

if $k_i > 0 \; or \; k_i < 0, \nabla k_i, i = 1,2 \dots,5.$ Then SEIR model always give eigenvalues are Real and complex. $\lambda_1 = a, \lambda_{2,3} = b \pm ci$ and $\lambda_{4,5} = b \pm ci$ with $a, b, c, d, e \in R$ and Stability analysis there are two, namely: Stable asymptotic and unstable.

## 3 Stability Analysis for Medan City

A parameter estimation performed in each population. Parameters and initial values mosquito populations used are the parameters of the results by [14] on Sulawesi. Because it is assumed that it has the same area that is endemic to dengue fever.

**Table 1** Parameter value spread of dengue fever

| Parameter Name | Notation | Value |
|---|---|---|
| The rate of recovery of humans infected with dengue virus | $\gamma_h$ | 0.328833 |
| The rate of human deaths caused by dengue virus | $\alpha_h$ | 0.0000002 |
| The rate of human infection with dengue virus | $\varphi_h$ | 0.16667 |
| Persentase nyamuk terinfeksi virus *dengue* | $P$ | 0.09 |
| The rate of mosquitoes infected with dengue virus | $\delta_v$ | 0.1428 |
| The rate of human deaths | $\mu_h$ | 0.000046 |
| Mosquito mortality rate | $\mu_v$ | 0.0323 |
| The rate of contact of humans to the vector | $b\beta_h$ | 0.75 |
| The rate of the vector-to-human contact | $b\beta_v$ | 0.375 |
| The number of births mosquitoes | $A = 1\% x\ N_h$ | 2899.56 |

$$N_h = 289956, \quad \alpha = \frac{\beta_h bA}{N_h \mu_v} = 0,232198142.$$

*3.1 Equilibrium Points for Medan City*

From equation (11-15) equilibrium model of SEIR the parameter values in the table above can be formulated as follows:

$$0,000046 - (0,090046 + 0,232198412z)x = 0$$
$$(0,09 \mp 0,232198412z)x - 0,166746u = 0$$
$$0,1667u - 0,3288792y = 0$$
$$0,375(1 - z - w)y - 0,1751w = 0$$
$$0,428w - 0,0323z = 0$$

By using the software MAPLE obtained equilibrium point value. For disease-free equilibrium point is as follows: $E_0 = (199,0599611, -0,0547635, -0,0277582, -0,087716, -0,3877971)$

Cannot be assessed because only $S_h$ value that is positive while the value of the other negative. This means it can be said $E_0$ unstable. Can be assessed by looking at its eigenvalues are:

$\lambda_1 = 0,6354942857$, $\lambda_2 = -0,1930171439 + 0,8220223055i$, $\lambda_3 = -0,0000093748$, $\lambda_4 = -1,023107911$, $\lambda_5 = -0,1930171439 - 0,822022306i$.

Because the equilibrium point is said to be unstable if one of the roots of the characteristic equation is real and positive, or if at least one root has a positive real part. For endemic equilibrium point $E_1 = (0,0005091, 0,0002757, 0,0001398, 0,0002988, 0,0013211)$ is an asymptotically stable equilibrium point. It can be assessed by looking at the eigenvalues of $E_1$ namely

$$\lambda_1 = -171292 + 0,0091331i, \qquad \lambda_2 = -0,0324563,$$
$$\lambda_3 = -0,0893149, \quad \lambda_4 = -0,3290751, \quad \lambda_5 = -0,1731091 - 0,87673321i.$$

Because the equilibrium point is said to be asymptotically stable if the roots of the characteristic equation are real and negative.

*3.2 Basic Reproduction Ratio*

Looking for $R_0$ value is important because it can show how much the infection will occur to individuals as a result of the infection. If a patient is free from dengue fever, $R_0 \leq 1$ value. If the patient can transmit to other individuals and more than one, the value $R_0 \geq 1$ and DFD endemic. According to [16], $R_0$ is the number of secondary cases generated by a vector-borne infectious cases in the whole population vulnerable. Mathematically defined as the dominant eigenvalues of the linear equation positive (constant). To determine the value $R_0$ so that we can take the constant of the characteristic equation (4.5) ie:

$$k_1 = 0, \qquad = \qquad C_1 C_2 C_3 (C_4 C_5 - C_6) = 0,$$
$$C_1 C_2 C_3 C_4 C_5 = C_1 C_2 C_3 C_6$$

$$\frac{C_4 C_5}{C_6} = 1$$

Thus, we have the basic reproduction ratio $R_0$ as follow:

$$R_0 = \frac{-hjm\left(\sqrt{q} - n\right)}{\left(-kh + hm\left(\sqrt{q} - n\right) + k + l\right)\left(\dfrac{hjlm(\sqrt{q} - n)}{-kh + hm\left(\sqrt{q} - n\right) + k + l} - j\right)}$$

By substituting the values of the parameters, the obtained value

$$R_0 = 2.46 \geq 1,$$

That means dengue fever does not disappear from the population and cause endemic in the district are Medan Helvetia and Medan Sunggal sub-disricts. So, every patient can transmit the dengue disease to more than one new case, so may cause more extensive disease.

*3.3 Numerical Simulation for Medan City*

In this section, Simulation of SEIR model of spread of dengue disease using data from the district and Sunggal Medan Medan Helvetia Medan sub-districts year 2013 to 2014.

**Table 2.** Data of DFD epidemic in Medan Helvetia and Medan Sunggal sub districts

| | 2013 | | | 2014 | | |
|---|---|---|---|---|---|---|
| | Medan Helvetia | Medan Sunggal | TOTAL | Medan Helvetia | Medan Sunggal | TOTAL |
| $S_h$ | 145.039 | 144.526 | 289.565 | 145.207 | 148.013 | 293.220 |
| $E_h$ | 5 | 9 | 14 | 7 | 24 | 31 |
| $I_h$ | 96 | 89 | 185 | 150 | 147 | 297 |
| $R_h$ | 99 | 93 | 192 | 155 | 176 | 331 |
| $N_h$ | 145.239 | 144.717 | 289.956 | 145.519 | 148.360 | 293.879 |

From the above table can be obtained initial conditions of population in 2013:

$$S_h(0) = x(0) = \frac{289565}{289956} = 0{,}998652$$

$$E_h(0) = u(0) = \frac{14}{289956} = 0{,}000048$$

$$I_h(0) = y(0) = \frac{185}{289956} = 0{,}000638$$

and the initial value used in vector population is the result of research [12], namely:
$$I_v(0) = w(0) = 0.01$$
$$E_v(0) = z(0) = 0.056$$

Based on that description, the spread of dengue fever can be written as follows. By the time interval [0, 30] and length of integration step h = 0.001. Suppose for:

$$\frac{dx}{dt} = 0,000046 - (0,090046 + 0,232198412z)x$$
$$= f_1(t, x, u, y, w, z),$$

$$\frac{du}{dt} = (0,09 + 0,232198412z)x - 0,166746u$$
$$= f_2(t, x, u, y, w, z)$$

$$\frac{dy}{dt} = 0,1667u - 0,3288792y$$
$$= f_3(t, x, u, y, w, z)$$

$$\frac{dw}{dt} = 0,375(1 - z - w)y - 0,1751w$$
$$= f_4(t, x, u, y, w, z)$$

$$\frac{dz}{dt} = 0,1428w - 0,0323z = f_5(t, x, u, y, w, z)$$

With initial value
$x_0 = 0,998652,$ $\quad u_0 = 0,000048,$
$y_0 = 0,000638,$ $\quad w_0 = 0,01,$ $\quad z_0 = 0,056.$
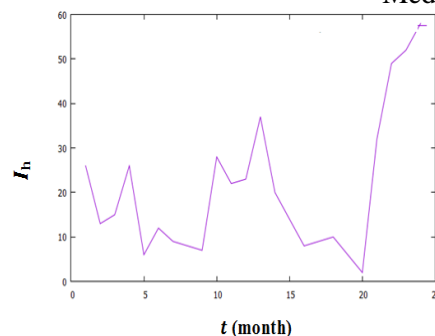
## 4. Results and Discussion

Graph data for 2013-2014 on $S_h$ population, $E_h$, and $I_h$, can be shown in figure 1, 2 and 3
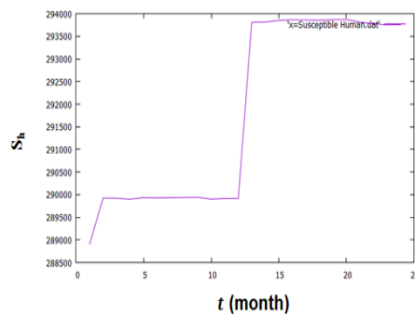


**Figure 1**. Graphs for Susceptible $S_h$ Population in Medan
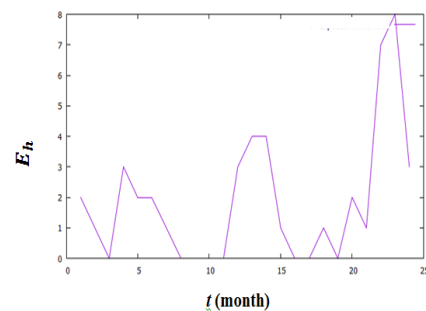


**Figure 2**. Graphs for Exposed $E_h$ Population in Medan



**Figure 3**. Graphs for Infected $I_h$ Population in Medan

In Figure 1 it can be seen that there is an increase and decrease very significantly. In Figure 2 $u_h$-class growth has decreased, this is due to $E_h$ class has moved into the class room $I_h$. And it can be seen in Figure 3 that an increase in the growth of human infected grade is high enough. This is because the Medan Helvetia and Medan Sunggal sub-districts the occurrence of endemic dengue disease.

**Table 3.** The Probability of SEIR model for DFD in year 2013-2014

| Year | $S_h$ | $E_h$ | $I_h$ | $E_v$ | $I_v$ |
|------|-------|-------|-------|-------|-------|
| 2013 | 0,9483166900 | 0,0486645532 | 0,0021747607 | 0,0093444069 | 0.0557868236 |
| 2014 | 0.0425493927 | 0.1065460550 | 0.0723738719 | 0.1244155478 | 0.3269441863 |

Graphs which were obtained by simulatiin for $S_h$, $E_h$, $I_h$, $E_v$, and $I_v$ can be shown in figure 5, 6, 7 and 8.
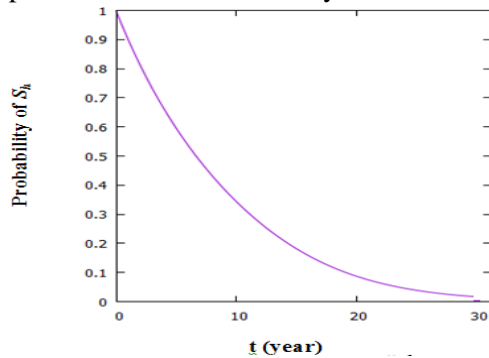


**Figure 4. Probability of $S_h$ through simulation**
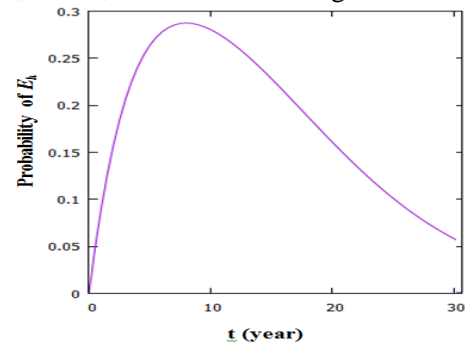


**Figure 5 Probability of $E_h$ through simulation**
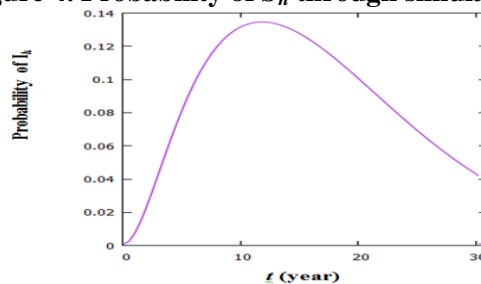


**Figure 6 Probability of $I_h$ through simulation**
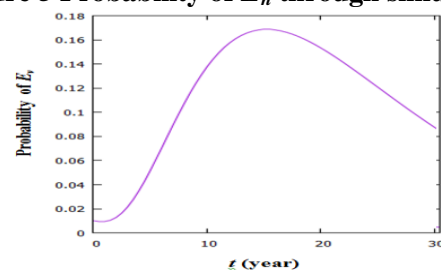


**Figure 7 Probability of $E_v$ through simulation**
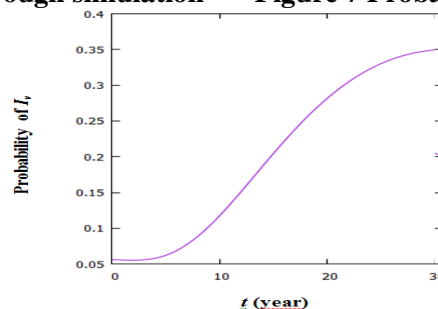


**Figure 8** Probability of $I_v$ through simulation

Based on Figure 4 shows that the rate class $S_h$ initially fell significantly to near 0 at $t = 30$. Reduced class as this $S_h$ due to the displacement of the class into groups and classes $E_h$ and $I_h$. In the Figure 5 The growth rate is reduced $E_h$ classes ranging from $t = 10$ due to the displacement of the class becomes class $I_h$ and $E_h$. Then the growth rate was reduced $I_h$. Then $S_h$ class condition, $E_h$, and $I_h$ will run continuously until toward an asymptotically stable point and at that point until $t \to \infty$. This means there is no spread of the virus dengeu in each class in the human population.

Based on Figure 7 shows that the growth rate is influenced by many $E_v$ class of vectors that bite humans infected with dengue virus. $I_v$ class growth rate initially rose significantly to exceed 0.25 in the initial time interval until 30 months. This is because of an infected of vector will continue to transmit during his lifetime. But the rate of growth of the running time seiringnya $E_v$ and $I_v$ classes is reduced so that the graph slowly down until toward an asymptotically stable point and at that point until $t \to \infty$. This means there is no spread of the virus dengue in each class in the vector population. This means that, in this population had no additional classes $I_v$ and $S_v$ which becomes infected vector.

From Figure (4, 5, 6, 7, 8), the growth rate $S_h$, $E_h$, $I_h$, $E_v$, and $I_v$ significant drop to near 0 in the initial time interval up to 30 months. This is because each class on the amount of human and vector populations are assumed equal. That is, every class that are susceptible will go to class exposed and infected.

1. Based on the above, the result is that dengue fever is endemic in Medan Helvetia and Medan Sunggal sub-districts. It is necessary for the eradication or termination of the chain of transmission of vector. Here are some of the efforts that can be done to break the chain of transmission of vector.

2. Protect yourself from vector bites. This can be done by installing netting on the windows, use vector repellent and insecticide in the form of a spray. Do 3M movements is shut water reservoirs, drain regular shelters and burying water cans or containers empty unused. This study gives results that dengue fever does not disappear from Medan Helvetia and Medan Sunggal sub-districts. This is consistent with the data from health center of the area where every year there is always a human infected.

## 5. Conclusion

Model SEIR in the spread of dengue fever has been analyzed. The analysis of SEIR model obtained: 1) The SEIR model have two points of equilibrium that are disease-free equilibrium point $E_0 = (199.0599611, -0.0547635, -0.0277582, -0.0877160, -0.3877971)$ and the endemic equilibrium point $E_1 = (0.0005091, 0.0002757, 0.0001398, 0.0002988, 0.0013211)$. Results of stability analysis $E_0$ unstable equilibrium point and $E_1$ asymptotically stable equilibrium point. 2) The value of Basic Reproduction Number $R_0 = 2.46 > 1$, which means that the local sub-district and sub-district of Medan Sunggal Helvetia is endemic area. This means that dengue fever will not be lost on those areas. $R_0 > 1$ indicate each patient can transmit the dengue disease to more than one new cases, so that the disease can spread more widely. 3) Numerical simulation on the spread of dengue fever using Runge-Kutta Order 4. Simulation the spread of dengue disease in SEIR models indicate a case of endemic, meaning that dengue fever is still present in the human and vector populations with time $t \rightarrow \infty$. Then the rate of growth of susceptible human class, Exposed human, human Infected, vector Exposed and Infected of vector will drop significantly to near 0 in the initial time interval to 30 years. This is because each class the number of human and vector populations are assumed equal. This means that every class that is on will enter the classroom susceptible exposed and infected. And there are many other epidemic mathematical model that can be developed. One of them is the model SEIRS. In the model SEIRS, later classes who have recovered can be infected with the same disease again.

## Acknowledgement

## References

[1]  Herbert, W. H, 2000, The Mathematics of Infectious Diseases, *Siam Rev.*, **42**, 4, pp. 599-653.

[2]  M. M. A. El-Sheikh and S. A. A. El-Marouf, 2004, On stability and bifurcation of solutions of an SEIR epidemic model with vertical transmission, *Inter. J. of Math. & Math. Sci*. **2004**, 56, pp. 2971-2987.

[3]  Al-Samadi, M., dan Gumah, G.N., 2014, On the Homotopy Analysis Method for Fractional SEIR Epidemic Model, *J. of App. Sci.*, **7**, 18, pp. 3809-3820.

[4]  Xue-Zhi Li and Bin Fang, 2009, Stability of an Age-structured SEIR Epidemic Model with Infectivity in Latent Period. *Applications and Applied Math.* **4**, 1, pp. 218 – 236

[5] Na Yi· , Qingling Zhang , Kun Mao, Dongmei Yang, Qin Li, 2009, Analysis and control of an SEIR epidemic system with nonlinear transmission rate. *Math. Comp. Model*. **50**, 9-10, pp. 1498-1513.

[6] Ma, Z., dan Jia, L., 2007, *Dynamical Modeling and Analysis of Epidemics,* World Scientific Publishing, Singapore.

[7] Li, J., dan Cui, N., 2013, Dynamic Analysis of an SEIR Model with Distinct Incidence for Exposed and Infectives, *Sci. World J.*, **2013**, 871393.

[8] Putra, T.R., 2011, Kestabilan Lokal Bebas Penyakit Model Epidemi SEIR Dengan Kemampuan Infeksi Pada Periode Laten, Infeksi, dan Sembuh, *Poli Rekayasa*, **7**, 1, 42-52.

[9] Kholisoh, S., Waluya, B., dan Kharis, M., 2012, Model Epidemi Pada Penyebaran Penyakit Campak dengan Pengaruh Vaksinasi, *UNNES J. of Math,* **1**, 2, 111-117

[10] M. El-Doma, 2013, Stability Analysis of a Size-Structured Population Model with Maturation Size and a Constant Inflow of Newborns. *Int. J. of Ecological Eco. Stat.***28**, 1.

[11] SANGARE Boureima, DIALLO Ouateni, SOME Longin, 2013, An Analysis of Stability and Convergence of A Finite-Difference Methods for One-Dimensional Partial Integro-Differential Equation Using A Moving Mesh. *Int. J. of Applied Math. Stat.*, **50**, 20.

[12] Side, S. and Noorani, M.S.M., 2013, A SIR model for spread of dengue fever disease (Simulation for South Sulawesi Indonesia and selangor Malaysia), *World J. of Model Simulation*, **9**, 2, pp. 96-105.

[13] Side, S. and Noorani, M.S.M., 2013, Lyapunov function of SIR and SEIR model for transmission of dengue fever disease., *Inter. J. of Simulation Proc. Model (IJSPM)*. **8**, 2/3, 177-184.

[14] Side, S. and Noorani, M.S.M., 2012, SEIR model for transmission of dengue fever, *Inter. J. of Adv. Sci. Eng. Inf. Tech.*, **9**, 1, 1-5.

[15] Rangkuti, Y.M., Sinaga M. S., Marpaung F., Side, S., 2014, A VSEIR model for transmission of Tuberculosis (TB) disease In north Sumatera, Indonesia, *AIP Conference proceedings*, **1635**, 201, doi : 10.1063/1.4903584.

[16] Diekmann O, Heesterbeek JA, & Metz JAJ, 1990. On the definition and the computation of the basic reproduction ratio R infectious diseases in heterogeneous populations. *J Math Biol*. **28**, pp. 365–382